



RAW SEQUENCE LISTING ERROR REPORT

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Application Serial Number: 09/466,778A
Source: 1600
Date Processed by STIC: 8/14/2003

RECEIVED

AUG 21 2003

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

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Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 04/24/2003



1600

RAW SEQUENCE LISTING

DATE: 08/14/2003

PATENT APPLICATION: US/09/466,778A

TIME: 15:07:38

Input Set : A:\PF487 subst. SL Aug2003.txt

Output Set: N:\CRF4\08142003\I466778A.raw

3 <110> APPLICANT: Hastings, et al.
5 <120> TITLE OF INVENTION: Novel Hyaluronan-Binding Proteins and Encoding Genes
7 <130> FILE REFERENCE: PF487
9 <140> CURRENT APPLICATION NUMBER: 09/466,778A
10 <141> CURRENT FILING DATE: 1999-12-20
12 <150> PRIOR APPLICATION NUMBER: 60/113,871
13 <151> PRIOR FILING DATE: 1998-12-23
15 <160> NUMBER OF SEQ ID NOS: 37
17 <170> SOFTWARE: PatentIn Ver. 2.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 6761
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
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29 <221> NAME/KEY: misc_feature
30 <222> LOCATION: (6342)
31 <223> OTHER INFORMATION: n equals a, t, g or c
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34 <221> NAME/KEY: misc_feature
35 <222> LOCATION: (6496)
36 <223> OTHER INFORMATION: n equals a, t, g or c
38 <220> FEATURE:
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44 <221> NAME/KEY: misc_feature
45 <222> LOCATION: (6535)
46 <223> OTHER INFORMATION: n equals a, t, g or c
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49 <221> NAME/KEY: misc_feature
50 <222> LOCATION: (6537)
51 <223> OTHER INFORMATION: n equals a, t, g or c
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54 <221> NAME/KEY: misc_feature
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56 <223> OTHER INFORMATION: n equals a, t, g or c
58 <220> FEATURE:
59 <221> NAME/KEY: misc_feature
60 <222> LOCATION: (6724)

Does Not Comply
Corrected Diskette Needed

pg 2, 6-7

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Input Set : A:\PF487 subst. SL Aug2003.txt

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 74 <221> NAME/KEY: misc_feature
 75 <222> LOCATION: (6753)
 76 <223> OTHER INFORMATION: n equals a, t, g or c
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 83 ggccacgcag acaggccggg tgttctgca gctgagggtc gccgtggcc atg atg gac 178
 84 Met Met Asp
 85 1
 87 cag ggc tgc cgg gaa atc ctt acc aca gcg ggc cct ttc acc gtg ctg 226
 88 Gln Gly Cys Arg Glu Ile Leu Thr Thr Ala Gly Pro Phe Thr Val Leu
 89 5 10 15
 91 gtg cca tcc gtc tcc tcc ttc tcc tcc agg acc atg aat gca tcc ctt 274
 92 Val Pro Ser Val Ser Ser Phe Ser Ser Arg Thr Met Asn Ala Ser Leu
 93 20 25 30 35
 95 gcc cag cag ctg tgt aga cag cac atc atc gca ggg cag cac atc ctg 322
 96 Ala Gln Gln Leu Cys Arg Gln His Ile Ile Ala Gly Gln His Ile Leu
 97 40 45 50
 99 gag gac aca agg acc caa caa aca cga agg tgg tgg acg ctg gcc ggg 370
 100 Glu Asp Thr Arg Thr Gln Gln Thr Arg Arg Trp Trp Thr Leu Ala Gly
 101 55 60 65
 103 cag gag atc acc gtc acc ttt aac caa ttc acg aaa tac tcc tac aag 418
 104 Gln Glu Ile Thr Val Thr Phe Asn Gln Phe Thr Lys Tyr Ser Tyr Lys
 105 70 75 80
 107 tac aaa gac cag ccc cag cag acg ttc aac atc tac aag gcc aac aac 466
 108 Tyr Lys Asp Gln Pro Gln Gln Thr Phe Asn Ile Tyr Lys Ala Asn Asn
 109 85 90 95
 111 ata gca gct aat ggc gtc ttc cac gtg gtc act ggc ctg cgg tgg cag 514
 112 Ile Ala Ala Asn Gly Val Phe His Val Val Thr Gly Leu Arg Trp Gln
 113 100 105 110 115
 115 gcc ccc tct ggg acc cct ggg gat ccc aag aga act atc gga cag atc 562
 116 Ala Pro Ser Gly Thr Pro Gly Asp Pro Lys Arg Thr Ile Gly Gln Ile
 117 120 125 130
 119 ctg gcc tct acc gag gcc ttc agc cgc ttt gaa acc atc ctg gag aac 610
 120 Leu Ala Ser Thr Glu Ala Phe Ser Arg Phe Glu Thr Ile Leu Glu Asn
 121 135 140 145
 123 tgt ggg ctg ccc tcc atc ctg gac gga cct ggg ccc ttc aca gtc ttt 658
 124 Cys Gly Leu Pro Ser Ile Leu Asp Gly Pro Gly Pro Phe Thr Val Phe
 125 150 155 160

*what about "n" at location
 6749?
 (see p.6)*

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127	gcc	cca	agc	aat	gag	gct	gtg	gac	agc	ttg	cgt	gac	ggc	cgc	ctg	atc	706
128	Ala	Pro	Ser	Asn	Glu	Ala	Val	Asp	Ser	Leu	Arg	Asp	Gly	Arg	Leu	Ile	
129		165					170						175				
131	tac	ctc	ttc	aca	gcg	ggt	ctc	tct	aaa	ctg	cag	gag	ttg	gtg	cgg	tac	754
132	Tyr	Leu	Phe	Thr	Ala	Gly	Leu	Ser	Lys	Leu	Gln	Glu	Leu	Val	Arg	Tyr	
133	180					185					190					195	
135	cac	atc	tac	aac	cac	ggc	cag	ctg	acc	gtt	gag	aag	ctc	atc	tcc	aag	802
136	His	Ile	Tyr	Asn	His	Gly	Gln	Leu	Thr	Val	Glu	Lys	Leu	Ile	Ser	Lys	
137				200					205					210			
139	ggt	cgg	atc	ctc	acc	atg	gcg	aac	cag	gtc	ctg	gct	gtg	aac	att	tct	850
140	Gly	Arg	Ile	Leu	Thr	Met	Ala	Asn	Gln	Val	Leu	Ala	Val	Asn	Ile	Ser	
141				215					220					225			
143	gag	gag	ggg	cgc	atc	ctg	ctg	gga	ccc	gag	ggg	gtc	ccg	ctg	cag	agg	898
144	Glu	Glu	Gly	Arg	Ile	Leu	Leu	Gly	Pro	Glu	Gly	Val	Pro	Leu	Gln	Arg	
145		230					235					240					
147	gta	gac	gtg	atg	gcc	gcc	aat	ggc	gtg	atc	cac	atg	ctg	gac	ggc	atc	946
148	Val	Asp	Val	Met	Ala	Ala	Asn	Gly	Val	Ile	His	Met	Leu	Asp	Gly	Ile	
149		245					250					255					
151	ctg	ctg	ccc	ccg	acc	atc	ctg	ccc	atc	ctg	ccc	aag	cac	tgc	agc	gag	994
152	Leu	Leu	Pro	Pro	Thr	Ile	Leu	Pro	Ile	Leu	Pro	Lys	His	Cys	Ser	Glu	
153	260					265					270				275		
155	gag	cag	cac	aag	att	gtg	gcg	ggc	tcc	tgt	gtg	gac	tgc	caa	gcc	ctg	1042
156	Glu	Gln	His	Lys	Ile	Val	Ala	Gly	Ser	Cys	Val	Asp	Cys	Gln	Ala	Leu	
157				280					285					290			
159	aac	acc	agc	acg	tgt	ccc	ccc	aac	agt	gtg	aag	ctg	gac	atc	ttc	ccc	1090
160	Asn	Thr	Ser	Thr	Cys	Pro	Pro	Asn	Ser	Val	Lys	Leu	Asp	Ile	Phe	Pro	
161				295					300					305			
163	aag	gag	tgt	gtc	tac	atc	cat	gac	cca	acg	ggg	ctc	aat	gtg	cta	aag	1138
164	Lys	Glu	Cys	Val	Tyr	Ile	His	Asp	Pro	Thr	Gly	Leu	Asn	Val	Leu	Lys	
165		310					315					320					
167	aag	ggc	tgt	gcc	agc	tac	tgc	aac	caa	acc	atc	atg	gaa	caa	ggc	tgc	1186
168	Lys	Gly	Cys	Ala	Ser	Tyr	Cys	Asn	Gln	Thr	Ile	Met	Glu	Gln	Gly	Cys	
169		325					330					335					
171	tgc	aaa	ggt	ttt	ttc	ggg	cct	gac	tgc	acg	cag	tgt	cct	ggg	ggc	ttc	1234
172	Cys	Lys	Gly	Phe	Phe	Gly	Pro	Asp	Cys	Thr	Gln	Cys	Pro	Gly	Gly	Phe	
173	340					345					350				355		
175	tcc	aac	ccc	tgc	tat	ggc	aaa	ggc	aat	tgc	agt	gat	ggg	atc	cag	ggc	1282
176	Ser	Asn	Pro	Cys	Tyr	Gly	Lys	Gly	Asn	Cys	Ser	Asp	Gly	Ile	Gln	Gly	
177				360					365					370			
179	aat	ggg	gcc	tgc	ctc	tgc	ttc	cca	gac	tac	aag	ggc	atc	gcc	tgc	cac	1330
180	Asn	Gly	Ala	Cys	Leu	Cys	Phe	Pro	Asp	Tyr	Lys	Gly	Ile	Ala	Cys	His	
181				375					380					385			
183	atc	tgc	tgc	aac	cca	aac	aag	cat	gga	gag	caa	tgc	cag	gaa	gac	tgc	1378
184	Ile	Cys	Ser	Asn	Pro	Asn	Lys	His	Gly	Glu	Gln	Cys	Gln	Glu	Asp	Cys	
185		390						395					400				
187	ggc	tgt	gtc	cat	ggt	ctc	tgc	gac	aac	cgc	cca	ggc	agt	ggg	ggg	gtg	1426
188	Gly	Cys	Val	His	Gly	Leu	Cys	Asp	Asn	Arg	Pro	Gly	Ser	Gly	Gly	Val	
189		405				410						415					
191	tgc	cag	cag	ggc	acg	tgt	gcc	cct	ggc	ttc	agt	ggc	cgg	ttc	tgc	aac	1474

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192 Cys Gln Gln Gly Thr Cys Ala Pro Gly Phe Ser Gly Arg Phe Cys Asn
193 420 425 430 435
195 gag tcc atg ggg gac tgt ggg ccc aca ggg ctg gcc cag cac tgc cac 1522
196 Glu Ser Met Gly Asp Cys Gly Pro Thr Gly Leu Ala Gln His Cys His
197 440 445 450
199 ctg cat gcc cgc tgt gtt agc cag gag ggt gtt gcc aga tgt cgc tgt 1570
200 Leu His Ala Arg Cys Val Ser Gln Glu Gly Val Ala Arg Cys Arg Cys
201 455 460 465
203 ctt gat ggc ttt gag ggt gat ggc ttc tcc tgc aca cct agc aac ccc 1618
204 Leu Asp Gly Phe Glu Gly Asp Gly Phe Ser Cys Thr Pro Ser Asn Pro
205 470 475 480
207 tgc tcc cac ccg gac cgt gga ggc tgc tca gag aat gct gag tgt gtc 1666
208 Cys Ser His Pro Asp Arg Gly Gly Cys Ser Glu Asn Ala Glu Cys Val
209 485 490 495
211 cct ggg tcc ctg ggc acc cac cag tgc aca tgc cac aaa ggc tgg agt 1714
212 Pro Gly Ser Leu Gly Thr His His Cys Thr Cys His Lys Gly Trp Ser
213 500 505 510 515
215 ggg gat ggc cgc gtc tgt gtg gct att gac gag tgt gag ctg gac gtg 1762
216 Gly Asp Gly Arg Val Cys Val Ala Ile Asp Glu Cys Glu Leu Asp Val
217 520 525 530
219 aga ggt ggc tgc cac acc gat gcc ctc tgc agc tat gtg ggc ccc ggg 1810
220 Arg Gly Gly Cys His Thr Asp Ala Leu Cys Ser Tyr Val Gly Pro Gly
221 535 540 545
223 cag agc cga tgc acc tgc aag ctg ggc ttt gcc ggg gat ggc tac cag 1858
224 Gln Ser Arg Cys Thr Cys Lys Leu Gly Phe Ala Gly Asp Gly Tyr Gln
225 550 555 560
227 tgc agc ccc atc gac ccc tgc cgg gca ggc aat ggc ggc tgc cac ggc 1906
228 Cys Ser Pro Ile Asp Pro Cys Arg Ala Gly Asn Gly Gly Cys His Gly
229 565 570 575
231 ctg gag ctg gag gca aat gcc cac ttc tcc atc ttc tac caa tgg ctt 1954
232 Leu Glu Leu Glu Ala Asn Ala His Phe Ser Ile Phe Tyr Gln Trp Leu
233 580 585 590 595
235 aag agt gcc ggc atc acg ctt cct gcc gac cgc cga gtc aca gcc ctg 2002
236 Lys Ser Ala Gly Ile Thr Leu Pro Ala Asp Arg Arg Val Thr Ala Leu
237 600 605 610
239 gtg ccc tcc gag gct gca gtc cgt cag ctg agc ccc gag gac cga gct 2050
240 Val Pro Ser Glu Ala Ala Val Arg Gln Leu Ser Pro Glu Asp Arg Ala
241 615 620 625
243 ttc tgg ctg cag cca agg acg ctg ccg aac ctg gtc agg gcc cat ttt 2098
244 Phe Trp Leu Gln Pro Arg Thr Leu Pro Asn Leu Val Arg Ala His Phe
245 630 635 640
247 ctc cag ggt gcc ctc ttc gag gag gag ctg gcc cgg ctg ggt ggg cag 2146
248 Leu Gln Gly Ala Leu Phe Glu Glu Glu Leu Ala Arg Leu Gly Gly Gln
249 645 650 655
251 gaa gtg gcc acc ctg aac ccc acc aca cgc tgg gag att cgc aac att 2194
252 Glu Val Ala Thr Leu Asn Pro Thr Thr Arg Trp Glu Ile Arg Asn Ile
253 660 665 670 675
255 agt ggg agg gtc tgg gtg cag aat gcc agc gtg gat gtg gct gac ctc 2242
256 Ser Gly Arg Val Trp Val Gln Asn Ala Ser Val Asp Val Ala Asp Leu

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257		680		685		690		
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260	Leu Ala Thr Asn Gly Val Leu His Ile Leu Ser Gln Val Leu Leu Pro							
261		695		700		705		
263	ccc cga ggg gat gtg ccc ggt ggg cag ggg ttg ctg cag cag ctg gac							2338
264	Pro Arg Gly Asp Val Pro Gly Gly Gln Gly Leu Leu Gln Gln Leu Asp							
265		710		715		720		
267	ttg gtg cct gcc ttc agc ctc ttc cgg gaa ttg ctg cag cac cat ggg							2386
268	Leu Val Pro Ala Phe Ser Leu Phe Arg Glu Leu Leu Gln His His Gly							
269		725		730		735		
271	ttg gtg ccc cag att gag gct gcc act gcc tac acc atc ttt gtg ccc							2434
272	Leu Val Pro Gln Ile Glu Ala Ala Thr Ala Tyr Thr Ile Phe Val Pro							
273	740		745		750		755	
275	acc aac cgc tcc ctg gag gcc cag ggc aac agc agt cac ctg gac gca							2482
276	Thr Asn Arg Ser Leu Glu Ala Gln Gly Asn Ser Ser His Leu Asp Ala							
277		760		765		770		
279	gac aca gtg cgg cac cat gtg gtc ctg ggg gag gcc ctc tcc atg gaa							2530
280	Asp Thr Val Arg His His Val Val Leu Gly Glu Ala Leu Ser Met Glu							
281		775		780		785		
283	acc ctg cgg aag ggt gga cac cgc aac tcc ctc ctg ggc cct gcc cac							2578
284	Thr Leu Arg Lys Gly Gly His Arg Asn Ser Leu Leu Gly Pro Ala His							
285		790		795		800		
287	tgg atc gtc ttc tac aac cac agt ggc cag cct gag gtg aac cat gtg							2626
288	Trp Ile Val Phe Tyr Asn His Ser Gly Gln Pro Glu Val Asn His Val							
289		805		810		815		
291	cca ctg gaa ggc ccc atg ctg gag gcc cct ggc cgc tcg ctg att ggt							2674
292	Pro Leu Glu Gly Pro Met Leu Glu Ala Pro Gly Arg Ser Leu Ile Gly							
293	820		825		830		835	
295	ctg tcg ggg gtc ctg acg gtg ggc tca agt cgc tgc ctg cat agc cac							2722
296	Leu Ser Gly Val Leu Thr Val Gly Ser Ser Arg Cys Leu His Ser His							
297		840		845		850		
299	gct gag gcc ctg cgg gag aaa tgt gta aac tgc acc agg aga ttc cgc							2770
300	Ala Glu Ala Leu Arg Glu Lys Cys Val Asn Cys Thr Arg Arg Phe Arg							
301		855		860		865		
303	tgc act cag ggc ttc cag ctg cag gac aca ccc agg aag agc tgt gtc							2818
304	Cys Thr Gln Gly Phe Gln Leu Gln Asp Thr Pro Arg Lys Ser Cys Val							
305		870		875		880		
307	tac cga tct ggc ttc tcc ttc tcc cgg ggc tgc tct tac aca tgt gcc							2866
308	Tyr Arg Ser Gly Phe Ser Phe Ser Arg Gly Cys Ser Tyr Thr Cys Ala							
309		885		890		895		
311	aag aag atc cag gtg cgg gac tgc tgc cct ggt ttc ttt ggc acg ctg							2914
312	Lys Lys Ile Gln Val Pro Asp Cys Cys Pro Gly Phe Phe Gly Thr Leu							
313	900		905		910		915	
315	tgt gag cca tgc cca ggg ggt cta ggg ggg gtg tgc tca ggc cat ggg							2962
316	Cys Glu Pro Cys Pro Gly Gly Leu Gly Gly Val Cys Ser Gly His Gly							
317		920		925		930		
319	cag tgc cag gac agg ttc ctg ggc agc ggg gag tgc cac tgc cac gag							3010
320	Gln Cys Gln Asp Arg Phe Leu Gly Ser Gly Glu Cys His Cys His Glu							
321		935		940		945		

09/466,778A 6

gaagcatgca cagggaggag accantttta ttgcttgtot ggttggatgg ggcaggaggg 6723
nctgagggcc tgtcccagac aatanhgtt cctcgag

6761

↓
location 6749

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:2; Xaa Pos. 2058,2109,2120,2122,2123
Seq#:4; N Pos. 1103,1257,1290,1296,1298,1449,1485,1509,1510,1511,1514
Seq#:4; Xaa Pos. 358,409,420,422,423
Seq#:5; Xaa Pos. 358,409,420,422,423
Seq#:7; N Pos. 36,51,248,508,521,564,933,945,951,958
Seq#:7; Xaa Pos. 44,131,135,149,265,272,276,278,281
Seq#:8; Xaa Pos. 44,131,135,149,265,272,276,278,281
Seq#:10; N Pos. 478,479,668,849,1138,1149,1157,1169,1172,1251
Seq#:10; Xaa Pos. 94,157,303,314,320,324,325,351
Seq#:11; Xaa Pos. 94,157,303,314,320,324,325,351
Seq#:18; N Pos. 40
Seq#:20; N Pos. 21
Seq#:26; N Pos. 40
Seq#:28; N Pos. 21
Seq#:34; N Pos. 40
Seq#:36; N Pos. 21